

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Ashkenazi, Avi
Chuntharapai, Anon
Kim, Kyung Jin

(ii) TITLE OF INVENTION: Apo-2 RECEPTOR

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Marschang, Diane L.
(B) REGISTRATION NUMBER: 35,600
(C) REFERENCE/DOCKET NUMBER: P1101P1

5 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-5416

(B) TELEFAX: 650/952-9881

(C) TELEX: 910/371-7168

10 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: Amino Acid

15 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
1 5 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
20 25 30

25 Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
35 40 45

Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
50 55 60

30 Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser
65 70 75

Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp
35 80 85 90

Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr
95 100 105

40 His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp
110 115 120

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Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
320 325 330

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Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
335 340 345

Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
350 355 360

15

Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
365 370 375

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
380 385 390

20

Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
395 400 405

25

Ala Asp Ser Ala Xaa Ser
410 411

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1799 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

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CGGCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC 100

CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145

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100

105

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110

115

75

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GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC 535
 Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr
 120 125 130

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AGA AAC ACA GTG TGT CAG TGC GAA GAA GGC ACC TTC CGG 574
 Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe Arg
 135 140 145

15

GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC ACA 613
 Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr
 150 155

GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA 652
 Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr
 160 165 170

CCC TGG AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC 691
 Pro Trp Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly
 175 180

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305

310

GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG 1120
 Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro
 315 320 325

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CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159
 Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys
 330 335 340

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GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198
 Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
 345 350

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TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237
 Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
 355 360 365

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GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276
 Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
 370 375

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CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315
 Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His
 380 385 390

TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
 Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
 395 400 405

5 GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400
Ala Asp Ser Ala Xaa Ser
410 411

10 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450

AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500
CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTCCTGCAC 1550

15 TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTGTTGTT TGGGATGTCA 1650

TTGTTTTTAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700

20 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAAG 1750

GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:3:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

35 GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGCACAATGA GATAAAGGTG 50

GCTAAAGCTG AGGCAGCGGG 70

5 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: Nucleic Acid

10 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

15

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:5:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30